

GenCore version 4.5
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On protein - protein search, using sw model

Run on: January 7, 2002, 16:03:54 : Search time 180.87 Seconds
(without alignments)
38.818 Million cell updates/sec

Title: US-08-569-749-10

Sequence: 1 PEQLASAGFYYVGNSDDVKG.....CWESGDDPWQHAKWEPRC 48

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 473505 secs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SPTRREMBL17:*

1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rhodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
1	294	100.0	1140	4 Q9UNH1
2	277	94.2	195	13 Q9IA10
3	277	94.2	197	13 Q9IA69
4	277	94.2	610	13 Q57319
5	276	93.9	602	11 Q9ESE9
6	270	91.8	589	11 Q9Q266
7	270	91.8	589	11 Q9ESE8
8	258	87.8	324	13 Q9DDE2
9	205	69.7	224	11 Q88424
10	202	68.7	264	12 Q9EN27
11	193	65.6	280	4 Q9AP71
12	193	65.6	281	12 Q9YIL8
13	193	65.6	298	4 Q9H2AB
14	191	65.0	276	12 Q89744
15	191	65.0	379	5 Q9U922
16	190	64.5	377	5 Q9NJ07
17	180	61.2	597	11 Q9R015
18	177	60.2	496	11 Q9E9F0
19	177	60.2	501	11 Q9EQ05

ALIGNMENTS

RESULT	1	Q9UNH1	PRELIMINARY:	PRY: 1140 AA.
ID	Q9UNH1			
AC	Q9UNH1;			
DT	01-MAY-2000	(TREMBL1, 13, Last sequence update)		
DT	01-JUN-2001	(TREMBL1, 17, Last annotation update)		
DE	AP12-MLT FUSION PROTEIN.			
GN	AP12-MLT.			
OS	Homo sapiens (Human).			
OC	EUkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MLIDINE-5927400; PubMed-10339464;			
RA	Dierlamm J., Baens M., Wlodarska I., Steffanova-Ouzounova M.,			
RA	Hernandez J.M., Bossfeld D.K., De Wolf-Peeters C., Hugemeijer A.,			
RA	Van den Berghe H., Marrynen P.,			
RT	*The apoptosis inhibitor gene AP12 and a novel 18q gene, MLT, are			
RT	recurrently rearranged in the t(11;18)(q21;q21) p65 associated with			
RT	mucosa-associated lymphoid tissue lymphomas.;			
RL	Blood 93:3601-3609 (1999).			
CC	-1 SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.			
DR	EMBL: AF230394; AAD61611; -.			
DR	HEMBL: Q13490; 1QH.			
DR	InterPro: IPR001370; BIR.			
DR	InterPro: IPR03576; Caspase.			
DR	InterPro: IPR01059; ICE-p20.			
DR	InterPro: IPR03398; Ig-C2.			
DR	InterPro: IPR00600; Ig-like.			
DR	InterPro: IPR00506; Ig-MHC.			
DR	PIR: PF00653; BIR; 3.			
DR	PIR: SM00228; BIR; 3.			
DR	SMART: SM01115; CASC; 1.			
DR	SMART: SM00408; IGC2; 1.			
DR	SMART: SM0410; Ig-like; 1.			
DR	PROSITE: PS0282; BIR_REPEAT_1; 3.			
DR	PROSITE: PS50208; CASPASE_P20; 1.			

PT	REPEAT	262	329	BIR REPEAT	3.	RC	TISSUE-KIDNEY;
PT	ZN FING	563	597	C3HC4-type		RA	Zn .. Denton M., Gu S.-M., Saikumar P., Venkatachalam M.A.;
SEQ	SEQUENCE	610 AA;	60924 MW;	AD47619600844A6	CRC64;	RT	*Cloning of cDNA for rat inhibitor of apoptosis protein 2. ";
Query Match	Best Local Similarity	94.2%	Score 277;	DB 13;	Length 610;	RL	Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
Matches	43; Conservative	89.6%	Pred. No. 2.9e-28;			CC	~- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
QY	1	PEQLASAGFVYVGNSDDWKCFCGCGGLRCRWESEGDPPWQHAKWPRCE	48			DR	EMBL: AP190020; AA04585_1; ..
DB	280	PEQLADAGFVYVGNSDDWKCFCGCGGLRCRWESEGDPPWQHAKWPRCE	327			DR	HSSP: 01340; JOBH;
RESULT	5					DR	InterPro: IPR001370; BIR.
ID	Q9E89	PRELIMINARY;	PRT;	602 AA.		DR	IPR01315; CARD.
AC	Q9E89;					DR	InterPro: IPR001841; Znf_fing.
DT	01-MAR-2001	(T-EMBLrel. 16, Created)				DR	PF0053; BIR; 3.
DT	01-MAR-2001	(T-EMBLrel. 16, Last sequence update)				DR	PFam: PF00619; CARD; 1.
RL						DR	PFam: PF00097; zf-C3HC4; 1.
CC	-1 SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.					DR	SMART; SM00238; BIR; 3.
DR	EMBL: AE103430; AAC22970_1; ..					DR	SMART; SM00114; CARD; 1.
DR	InterPro: IPR001370; BIR.					DR	SMART; SM00184; RING; 1.
DR	InterPro: IPR001315; CARD.					DR	PROSITE: PS50143; BIR_REPEAT_1; 3.
DR	InterPro: IPR001841; Znf_fing.					DR	PROSITE: PS50209; CARD; 1.
DR	Pfam: PF00653; BIR; 3.					KW	Zinc-finger.
DR	Pfam: PF00619; CARD; 1.					SO	SEQUENCE FROM N.A.
DR	Pfam: PF00097; zf-C3HC4; 1.					SO	SEQUENCE 589 AA; 66777 MW; B6812FPE3A34142 CRC64;
DR	SMART; SM00238; BIR; 3.					Query Match	Best Local Similarity 91.8%; Score 270; DB 11; Length 589; Matches 42; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
DR	SMART; SM00114; CARD; 1.					QY	1 PEQLASAGFVYVGNSDDWKCFCGCGGLRCRWESEGDPPWQHAKWPRCE
DR	SMART; SM00184; RING; 1.					DB	48
DR	SMART; SM00184; RING; 1.					259 PEQLASAGFVYVGNSDDWKCFCGCGGLRCRWESEGDPPWQHAKWPRCE	
DR	SMART; PS01282; BIR_REPEAT_1; 1.						306
DR	PROSITE; PS50143; BIR_REPEAT_2; 3.						
DR	PROSITE; PS50209; CARD; 1.						
DR	Zinc-finger.						
SO	SEQUENCE 602 AA; 67326 MW; CC9138BEEA2D05A CRC64;						
Query Match	Best Local Similarity	93.9%; Score 276;	DB 11;	Length 602;			
Matches	43; Conservative	89.6%; Pred. No. 3.9e-28;					
QY	1	PEQLASAGFVYVGNSDDWKCFCGCGGLRCRWESEGDPPWQHAKWPRCE	48				
DB	273	PEQLASAGFVYVGNSDDWKCFCGCGGLRCRWESEGDPPWQHAKWPRCE	320				
RESULT	6						
ID	Q9QZG6	PRELIMINARY;	PRT;	589 AA.			
AC	Q9QZG6;						
DT	01-MAY-2000	(T-EMBLrel. 13, Created)					
DT	01-MAY-2000	(T-EMBLrel. 13, Last sequence update)					
DT	01-JUN-2001	(T-EMBLrel. 17, Last annotation update)					
DE	INHIBITOR OF APOPTOSIS PROTEIN 2.						
DR	EMBL: AP18431; AAC22971_1; ..						
DR	InterPro: IPR001370; BIR.						
DR	InterPro: IPR001315; CARD.						
DR	InterPro: IPR001841; Znf_fing.						
DR	Pfam: PF00653; BIR; 3.						
DR	Pfam: PF00619; CARD; 1.						
DR	Pfam: PF00097; zf-C3HC4; 1.						
DR	SMART; SM00114; CARD; 1.						
DR	SMART; SM00184; RING; 1.						
DR	SMART; PS01282; BIR_REPEAT_1; 1.						
DR	PROSITE; PS50143; BIR_REPEAT_2; 3.						
DR	PROSITE; PS50209; CARD; 1.						
DR	Zinc-finger.						
SO	SEQUENCE 589 AA; 66750 MW; B4F7089HD7CD285B CRC64;						
Query Match	Best Local Similarity	91.8%; Score 270;	DB 11;	Length 589;			
Matches	42; Conservative	87.5%; Pred. No. 2.4e-27;					
QY	1	PEQLASAGFVYVGNSDDWKCFCGCGGLRCRWESEGDPPWQHAKWPRCE	48				
DB							
RESULT	7						
ID	Q9E89	PRELIMINARY;	PRT;	589 AA.			
AC	Q9E89;						
DT	01-MAR-2001	(T-EMBLrel. 16, Created)					
DT	01-MAR-2001	(T-EMBLrel. 16, Last sequence update)					
DE	INHIBITOR OF APOPTOSIS PROTEIN 2.						
DR	EMBL: AP18431; AAC22971_1; ..						
DR	InterPro: IPR001370; BIR.						
DR	InterPro: IPR001315; CARD.						
DR	InterPro: IPR001841; Znf_fing.						
DR	Pfam: PF00653; BIR; 3.						
DR	Pfam: PF00619; CARD; 1.						
DR	Pfam: PF00097; zf-C3HC4; 1.						
DR	SMART; SM00114; CARD; 1.						
DR	SMART; SM00184; RING; 1.						
DR	SMART; PS01282; BIR_REPEAT_1; 1.						
DR	PROSITE; PS50143; BIR_REPEAT_2; 3.						
DR	PROSITE; PS50209; CARD; 1.						
DR	Zinc-finger.						
SO	SEQUENCE 589 AA; 66750 MW; B4F7089HD7CD285B CRC64;						
Query Match	Best Local Similarity	91.8%; Score 270;	DB 11;	Length 589;			
Matches	42; Conservative	87.5%; Pred. No. 2.4e-27;					
QY	1	PEQLASAGFVYVGNSDDWKCFCGCGGLRCRWESEGDPPWQHAKWPRCE	48				
DB							
RESULT	8						
ID	Q9E89	PRELIMINARY;	PRT;	589 AA.			
AC	Q9E89;						
DT	01-MAR-2001	(T-EMBLrel. 16, Created)					
DT	01-MAR-2001	(T-EMBLrel. 16, Last sequence update)					
DE	INHIBITOR OF APOPTOSIS PROTEIN 2.						
DR	EMBL: AP18431; AAC22971_1; ..						
DR	InterPro: IPR001370; BIR.						
DR	InterPro: IPR001315; CARD.						
DR	InterPro: IPR001841; Znf_fing.						
DR	Pfam: PF00653; BIR; 3.						
DR	Pfam: PF00619; CARD; 1.						
DR	Pfam: PF00097; zf-C3HC4; 1.						
DR	SMART; SM00114; CARD; 1.						
DR	SMART; SM00184; RING; 1.						
DR	SMART; PS01282; BIR_REPEAT_1; 1.						
DR	PROSITE; PS50143; BIR_REPEAT_2; 3.						
DR	PROSITE; PS50209; CARD; 1.						
DR	Zinc-finger.						
SO	SEQUENCE 589 AA; 66750 MW; B4F7089HD7CD285B CRC64;						
Query Match	Best Local Similarity	91.8%; Score 270;	DB 11;	Length 589;			
Matches	42; Conservative	87.5%; Pred. No. 2.4e-27;					
QY	1	PEQLASAGFVYVGNSDDWKCFCGCGGLRCRWESEGDPPWQHAKWPRCE	48				
DB							
RESULT	9						
ID	Q9QZG6	PRELIMINARY;	PRT;	589 AA.			
AC	Q9QZG6;						
DT	01-MAY-2000	(T-EMBLrel. 13, Created)					
DT	01-MAY-2000	(T-EMBLrel. 13, Last sequence update)					
DT	01-JUN-2001	(T-EMBLrel. 17, Last annotation update)					
DE	INHIBITOR OF APOPTOSIS PROTEIN 2.						
DR	EMBL: AP18431; AAC22971_1; ..						
DR	InterPro: IPR001370; BIR.						
DR	InterPro: IPR001315; CARD.						
DR	InterPro: IPR001841; Znf_fing.						
DR	Pfam: PF00653; BIR; 3.						
DR	Pfam: PF00619; CARD; 1.						
DR	Pfam: PF00097; zf-C3HC4; 1.						
DR	SMART; SM00114; CARD; 1.						
DR	SMART; SM00184; RING; 1.						
DR	SMART; PS01282; BIR_REPEAT_1; 1.						
DR	PROSITE; PS50143; BIR_REPEAT_2; 3.						
DR	PROSITE; PS50209; CARD; 1.						
DR	Zinc-finger.						
SO	SEQUENCE 589 AA; 66750 MW; B4F7089HD7CD285B CRC64;						
Query Match	Best Local Similarity	91.8%; Score 270;	DB 11;	Length 589;			
Matches	42; Conservative	87.5%; Pred. No. 2.4e-27;					
QY	1	PEQLASAGFVYVGNSDDWKCFCGCGGLRCRWESEGDPPWQHAKWPRCE	48				
DB							
RESULT	10						
ID	Q9QZG6	PRELIMINARY;	PRT;	589 AA.			
AC	Q9QZG6;						
DT	01-MAY-2000	(T-EMBLrel. 13, Created)					
DT	01-MAY-2000	(T-EMBLrel. 13, Last sequence update)					
DT	01-JUN-2001	(T-EMBLrel. 17, Last annotation update)					
DE	INHIBITOR OF APOPTOSIS PROTEIN 2.						
DR	EMBL: AP18431; AAC22971_1; ..						
DR	InterPro: IPR001370; BIR.						
DR	InterPro: IPR001315; CARD.						
DR	InterPro: IPR001841; Znf_fing.						
DR	Pfam: PF00653; BIR; 3.						
DR	Pfam: PF00619; CARD; 1.						
DR	Pfam: PF00097; zf-C3HC4; 1.						
DR	SMART; SM00114; CARD; 1.						
DR	SMART; SM00184; RING; 1.						
DR	SMART; PS01282; BIR_REPEAT_1; 1.						
DR	PROSITE; PS50143; BIR_REPEAT_2; 3.						
DR	PROSITE; PS50209; CARD; 1.						
DR	Zinc-finger.						
SO	SEQUENCE 589 AA; 66750 MW; B4F7089HD7CD285B CRC64;						
Query Match	Best Local Similarity	91.8%; Score 270;	DB 11;	Length 589;			
Matches	42; Conservative	87.5%; Pred. No. 2.4e-27;					
QY	1	PEQLASAGFVYVGNSDDWKCFCGCGGLRCRWESEGDPPWQHAKWPRCE	48				
DB							

SEQUENCE FROM N.A.

RATTUS NORVEGICUS (rat).

OC Bokayora; Chodat; Craniata; Vertebrata; Buteleostomi; Mammalia; Etheridia; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

NCBI-TAXID=1016;

[1]

SEQUENCE FROM N.A.

[1] R N
RP SEQUENCE FROM N.A.
RX MEDLINE-9837638; PubMed=9712513;
RA Hu Z.H., Arif B.M., Sun J.S., Chen X.W., Zuidema D., Goldbach R.W.,

Search completed: January 7, 2002, 16:03:54
Job time: 1413 sec

Query Match 276 AA: 31617 MN: C467275B5B3642 CRC64;							
Best Local Similarity 63.8%; Matches 30; Conservative 5; Mismatches 12; Indels 0; Gaps 0;		Score 191; DB 12; Length 276; Pred. No. 2.6e-17; Mismatches 12; Indels 0; Gaps 0;		Query Match 65.0%; Score 191; DB 12; Length 276; Pred. No. 3.7e-17; Mismatches 12; Indels 0; Gaps 0;			
QY	DB	1 PEQLASAGFYYVGNNSDVKFCGCGGLRCWSSGDDPWWOHAKWPRC 47	127 PEQLADAGFYYVQGSDKTCFRCNGGLKDWDGDEPWWOHARWFNC 173	QY	DB	1 PEQLASAGFYYVGNNSDVKFCGCGGLRCWSSGDDPWWOHAKWPRC 47	127 PEQLADAGFYYVQGSDKTCFRCNGGLKDWDGDEPWWOHARWFNC 173
RESULT	15	.	.	RESULT	15	.	.
Q9U492	Q9U492	PRELIMINARY;	PRT;	Q9U492	Q9U492	PRELIMINARY;	PRT;
ID	ID	09U492	09U492	ID	ID	09U492	09U492
AC	AC	09U492;	PRT;	AC	AC	09U492;	PRT;
DT	DT	01-MAY-2000	01-MAY-2000	DT	DT	01-MAY-2000	01-MAY-2000
TR	TR	{TREMBLrel.	{TREMBLrel.	TR	TR	{TREMBLrel.	{TREMBLrel.
13,	13,	Created)	13,	13,	13,	Created)	13,
DE	DE	01-JUN-2001	01-JUN-2001	DE	DE	01-JUN-2001	01-JUN-2001
INHIBITOR OF APOPTOSIS PROTEIN.	INHIBITOR OF APOPTOSIS PROTEIN.			INHIBITOR OF APOPTOSIS PROTEIN.	INHIBITOR OF APOPTOSIS PROTEIN.		
IAPI.	IAPI.			IAPI.	IAPI.		
TRICHOPLUSIA NI (Cabbage Looper)	TRICHOPLUSIA NI (Cabbage Looper)			TRICHOPLUSIA NI (Cabbage Looper)	TRICHOPLUSIA NI (Cabbage Looper)		
Arthropoda; Tracheata; Hexapoda; Insecta;	Arthropoda; Tracheata; Hexapoda; Insecta;			Arthropoda; Tracheata; Hexapoda; Insecta;	Arthropoda; Tracheata; Hexapoda; Insecta;		
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;		
PTERYGOTA; NEOPTERA; ENDOPTERYGOTA; LEPIDOPTERA; GLOSSATA; DITRYSIA;	PTERYGOTA; NEOPTERA; ENDOPTERYGOTA; LEPIDOPTERA; GLOSSATA; DITRYSIA;			PTERYGOTA; NEOPTERA; ENDOPTERYGOTA; LEPIDOPTERA; GLOSSATA; DITRYSIA;	PTERYGOTA; NEOPTERA; ENDOPTERYGOTA; LEPIDOPTERA; GLOSSATA; DITRYSIA;		
Noctuidae; Noctuidae; Plusiinae; Trichoplusia.	Noctuidae; Noctuidae; Plusiinae; Trichoplusia.			Noctuidae; Noctuidae; Plusiinae; Trichoplusia.	Noctuidae; Noctuidae; Plusiinae; Trichoplusia.		
NCBI_TAXID>711;	NCBI_TAXID>711;			NCBI_TAXID>711;	NCBI_TAXID>711;		
[1]	[1]			[1]	[1]		
SEQUENCE FROM N_A.	SEQUENCE FROM N_A.			SEQUENCE FROM N_A.	SEQUENCE FROM N_A.		
RP	RP	MEDLINE=>20063908; PUBMED=>10593985;	RP	RP	RP	MEDLINE=>20063908; PUBMED=>10593985;	RP
RA	RA	Seshagiri S.; Vuicic D.; Lee J.; Dixit V.M.;	RA	RA	RA	Seshagiri S.; Vuicic D.; Lee J.; Dixit V.M.;	RA
RT	RT	'Baculovirus-based genetic screen for antiapoptotic genes identifies a novel IAP.'	RT	RT	RT	'Baculovirus-based genetic screen for antiapoptotic genes identifies a novel IAP.'	RT
RL	RL	J. Biol. Chem. 274:36759-36773(1999).	RL	RL	RL	J. Biol. Chem. 274:36759-36773(1999).	RL
EMBL; AF019558; AF19819.1; -.	EMBL; AF019558; AF19819.1; -.	EMBL; AF019558; AF19819.1; -.	EMBL; AF019558; AF19819.1; -.	EMBL; AF019558; AF19819.1; -.	EMBL; AF019558; AF19819.1; -.	EMBL; AF019558; AF19819.1; -.	EMBL; AF019558; AF19819.1; -.
DR	DR	HS3P; Q13490; 1QH.	DR	DR	DR	HS3P; Q13490; 1QH.	DR
InterPro:	InterPro:	IPR011670; BIR.	InterPro:	InterPro:	InterPro:	IPR011670; BIR.	InterPro:
InterPro:	InterPro:	IPR01841; 2nf_ring.	InterPro:	InterPro:	InterPro:	IPR01841; 2nf_ring.	InterPro:
PFAM:	PFAM0653;	BIR; 2.	PFAM:	PFAM0653;	PFAM:	PFAM0653;	PFAM:
SMART:	SMART:	SM0028; BIR; 2.	SMART:	SMART:	SMART:	SM0028; BIR; 2.	SMART:
PROSITE:	PROSITE:	PS01282; BIR; 1.	PROSITE:	PROSITE:	PROSITE:	PS01282; BIR; REPEAT_2; 2.	PROSITE:
SEQUENCE:	SEQUENCE:	SEQUENCE_39 AA; 41857 MN; 069381A012D9DE65 CRC64;	SEQUENCE:	SEQUENCE:	SEQUENCE:	SEQUENCE_39 AA; 41857 MN; 069381A012D9DE65 CRC64;	SEQUENCE:

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